

Serial No. 10/683,535

PATENT
Docket No. 58027-014000**AMENDMENTS TO THE CLAIMS**

Claim 1 (original): A constraint-based method for identifying a genomic target of interest from gene expression profiles, comprising:

- obtaining tissue sample expression data sets;
- selecting a working gene-expression set, said gene-expression set having a plurality of members;
- defining subgroups of said tissue samples of said expression data sets, wherein said subgroup definition is a constrained definition; and
- analyzing co-expression of said members of said working gene set across said subgroups and identifying potential gene targets.

Claim 2 (withdrawn): The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets from tumor samples.

Claim 3 (original): The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets from tissue from a mammal.

Claim 4 (withdrawn): The method of claim 3, wherein said tissue sample expression data sets are comprised of expression data sets attained tissue from at least one of a human, mouse, primate, canine, pig, rat, and feline.

Claim 5 (withdrawn): The method of claim 1, wherein said tissue sample expression data sets are comprised of expression data sets based upon tissue from an embryo.

Claim 6 (withdrawn): The method of claim 2, wherein said tumor are breast cancer tumors.

Claim 7 (withdrawn): The method of claim 2 wherein said tumors are cancer tumors of the digestive tract.

Claim 8 (original): The method of claim 1, wherein said working gene expression set comprises at least one receptor tyrosine kinase.

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Claim 9 (withdrawn): The method of claim 1, wherein said working gene expression set comprises a receptor and a ligand.

Claim 10 (original): The method of claim 1, further comprising a step of selecting known prognostic markers that are correlative with prognostic outcomes.

Claim 11 (original): The method of claim 1, further comprising a step of binning said working gene-expression set.

Claim 12 (withdrawn): A constraint-based method for analysis of gene expression profiles, comprising:

- selecting a working gene set;
- investigating expression patterns of said working gene set in a set of tissue samples;
- defining cutting values to define categories of gene expression levels; selecting constraints in order to bin said tissue samples into groups according to gene expression;
- investigating the frequency of up-regulated and down-regulated genes across individual members and groups; and
- forming at least one matrix which provides a basis for investigation of expression of members of said working gene set across said set of tissue samples, thereby providing at least one potential gene target.

Claim 13 (withdrawn): The method of claim 12, wherein said investigation includes calculating an intensity ratio of a particular gene of said working gene set, said intensity ratio calculated by comparison of a particular gene expression intensity to a calculated average intensity.

Claim 14 (withdrawn): The method of claim 13, wherein said intensity ratio is utilized to provide information utilized to construct at least a part of at least one matrix, said matrix being comprised of a plurality of calculated ratios.